

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 ctgggagtgga tatggagtgg tggaaatcaca gactataatg cagctttcat atccagactg 660
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 ggctcggggc gtgtgtgggtc ctacacagagc ctgtccatca cctgcacagt gaagcagctca 480
 ggaactggcc tagtgcagtc acactgggtt cgccagctctc cagtaaaggg tctgggtttc 540
 tcattaaacta cctatctgtg acactgggtt gactataatg cagctttcat atccagactg 600
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 <212> DNA
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 ctgggagtgga tatggagtgg tggaaatcaca caagagccaa gtcacgtct cctctgatct 660
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 aatgacacag ccatttatta actgggtgca aggaactca agccagcag cctctgatct 780
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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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accaagaacc aggtcagcct gacctgctgt gtcacaggtc tctatccagc cgcacatcgcc 1320
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgac tcccggtgctg 1380
gactccgacg gctcctctct cctctacagc aagctcacgc tggacaagag cagggtggcag 1440
caggggagac gctctctatg ctccgtgtag catgaggctc tgcacaacca ctacacgcag 1500
aagagccctc cctctgctcc gggtaaaagc gatccttcga acctgctccc atcctgggccc 1560
attactctaa tctcagtaaa tgggaatttt gtgatatgct gcctgacctc ctgctttggc 1620
ccaagatgca gagagagaag gaggaatgag agattgagaa gggaaagtgt acgcccctga 1680
taaatcgata ctcgag 1696

<210> 359
<211> 141
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 359
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Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln
20 25 30
Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45
Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
50 55 60
Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala
65 70 75
Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Ser Lys Ser Gln
80 85 90
Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr
100 105 110
Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr Ala Met
115 120 125
Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135 140

<210> 360
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 360
Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Ser Ser Gln
1 5 10 15
Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
20 25 30
Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45
Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala Ala Phe Ile
50 55 60
Ser Arg Leu Ser Ile Thr Lys Asp Ser Lys Ser Gln Val Phe Phe
65 70 75
Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
80 85 90
Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr Ala Met Asp Tyr Trp
100 105 110
Gly Gln Gly Thr Ser Val Thr Val Ser Ser

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
115 120

<210> 361
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 361
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Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg
130

<210> 362
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 362
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
 210 215 220
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
 225 230 235 240
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 260 265 270

<210> 363
 <211> 505
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> fusion polypeptide

<400> 363
 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
 1 5 10 15
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
 20 25 30
 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
 35 40 45
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 85 90 95
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 105 110
 Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
 115 120 125
 Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 130 135 140
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
 145 150 155 160
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
 165 170 175
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
 180 185 190
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
 195 200 205
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
 210 215 220
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
 225 230 235 240
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 265 270
 Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Ser Pro
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 330 335
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 340 345 350
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 355 360 365
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 370 375 380
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys
500 505

<210> 364
<211> 556
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 364
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
160 165 170
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
175 180 185
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
190 195 200
Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Ser Lys
205 210 215
Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
220 225 230
Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
235 240 245
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
250 255 260
Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
265 270 275
Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys
280 285 290
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
295 300 305
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Thr Tyr
310 315 320
325 330 335

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Ser Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 425 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu
500 505 510
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile
515 520 525
Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
530 535 540 545
Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
545 550 555

<210> 365
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to Y

<400> 365
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gtagaaggag cc 72

<210> 366
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A

<400> 366
gttggtgaag acgttccct gctgccacct gctctgtgcc acggtgagct tgctgtagag 60
ggcgaaggag cc 72

<210> 367
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
407 XX to A

<400> 367

WO 2005/037989

PT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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gaagaaggag cc 72

<210> 368
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to Y and 407 to A

<400> 368
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gtagaaggag cc 72

<210> 369
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A and 407 to Y

<400> 369
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ggcgaaggag cc 72

<210> 370
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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tgggagagca atgggcagcc ggagaacaac tacaagacca cgcttccgt gctggactcc 180
gacggctcct tctacctcta tagcaagctc accgtggaca agagcagggt gcagcagggg 240
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<210> 371
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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tgggagagca atgggcagcc ggagaacaac tacaagacca cgcttccgt gctggactcc 180
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ctctccctgt ccccggttaa atga 324

<210> 372
<211> 324
<212> DNA
<213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>

<223> fusion polynucleotide

<400> 372

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tgggagagca  atgggcagcc  ggagaaacaac  tacaagacca  cgcctcccg  gctggactcc  180
gacggtctct  ctctctcgc  cagcaagctc  accgtggaca  agagcagggt  gcagcagggg  240
aacgtcttct  catgctccgt  gatgcatgag  gctctgcaca  accactacac  gcagaagagc  300
ctctccctgt  ccccgggtaa  atga
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<210> 373

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 373

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tgggagagca  atgggcagcc  ggagaaacaac  tacaagacca  cgcctcccg  gctggactcc  180
gacggtctct  ctctctcgc  cagcaagctc  accgtggaca  agagcagggt  gcagcagggg  240
aacgtcttct  catgctccgt  gatgcatgag  gctctgcaca  accactacac  gcagaagagc  300
ctctccctgt  ccccgggtaa  atga
                                     324
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<210> 374

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 374

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tgggagagca  atgggcagcc  ggagaaacaac  tacaagacca  cgcctcccg  gctggactcc  180
gacggtctct  ctctctcgc  cagcaagctc  accgtggaca  agagcagggt  gcagcagggg  240
aacgtcttct  catgctccgt  gatgcatgag  gctctgcaca  accactacac  gcagaagagc  300
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<210> 375

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 375

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20     25     30
Tyr  Pro  Ser  Asp  Ile  Ala  Val  Glu  Trp  Glu  Ser  Asn  Gly  Gln  Pro  Glu
35     40     45
Asn  Asn  Tyr  Lys  Thr  Thr  Pro  Pro  Val  Leu  Asp  Ser  Asp  Gly  Ser  Phe
50     55     60
Tyr  Leu  Tyr  Ser  Lys  Leu  Thr  Val  Asp  Lys  Ser  Arg  Trp  Gln  Gln  Gly
65     70     75     80
Asn  Val  Phe  Ser  Cys  Ser  Val  Met  His  Glu  Ala  Leu  His  Asn  His  Tyr
85     90     95
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WO 2005/037989

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 376
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> fusion polypeptide

<400> 376
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Ala Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 377
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> fusion polypeptide

<400> 377
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Phe Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 378
<211> 107
<212> PRT
<213> Artificial Sequence
<220>
<223> fusion polypeptide

<400> 378
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 20 25 30
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60
 Tyr Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 100 105

<210> 379
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 379
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 1 5 10 15
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 20 25 30
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45
 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60
 Ala Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 100 105

<210> 380
 <211> 1515
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 380
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 gtacataattg ccaggggaca aattgtcttc tccagctctc cagcaattct gtctgcatct 120
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
 taccagcaga agccaggatc ctcccccaaa cctctggatt atgcccactc caacctcgtg 240
 tctggagctc ctgcttcgct cagttggcagt gggtctggga cctctctact tctcaacaac 300
 agcagagtggt aggtctgaaga tgctgccact tattactgcc agcagtgtag ctttaaccaca 360
 cccacgtctcg gtctctgggac caagctggag ctgaaagatg gcggtggctc ggcgcgtggg 420
 gggatctggag gagggtgggag ctctcaggct tatctacagc agtctggggc tggagctggg 480
 aggcctgggg cctcagtgaa gatgtcctgc aaggctctctg gctacacatt taccagttac 540
 aatatgcact gggtaaaagca gacacctaga cagggtcctg aatggattgg agctatttat 600
 ccaggaaattg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaaatcct gcagcacagc ctacatgcag ctccagcagc tgacatctga agactctcgg 720
 gtctatttct ctgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
 ggacacaggga ccacgtctcc cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840
 cacacatccc caaggacac agcacctgaa ctctctgggg gaccgtcagt ctctctcttc 900
 ccccaaaaac cctcatgata tcccgagacc ctgaggctcac atgcgtgggt 960
 gtggagctga gccacgaaga ccttgaggac aagttcaact ggtacgtgga cggcgtggag 1020
 gtgcataatg ccaagacaaa ccgcgaggag gaggagtaca acagcacgta cgtgtgggtc 1080
 agcgtcctca cgtctctgca ccaggactgg ctgaaatggca agggagtacaa gtgcaaggct 1140

WO 2005/037989

PCT/US2003/024918

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 tccaacaaga ccttcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
 cgagaaccac aggtgttacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1260
 agccttgacct agcttggtaaa aggtcttctat cccagcgaca gtgggagagc 1320
 aatggggcagc cggagaacaa ctacaagacc acgctctccc tgctggagtc cgacggctcc 1380
 ttgcgctctc atagcaagct caccgtggag aagagcaggt ggcagcaggg gaacgtcttc 1440
 tcatgtcccg tgatgcatga ggctctgcac aaccactaca cgagaagag cctctccctg 1500
 tccccgggta aatga
 1515

<210> 381
 <211> 1521
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

<400> 381
 aagcttgccg ccattggatt tcaagtgcag attttcagct tcctgctaag cagtgtctta 60
 gtcataattg aggtcacaat gacttcgagg gccagctcaa gtgtaagta gctgtcatct 120
 ccaggggaga aggtcacaat ctccccaa ccttggatt atgccccat caactggctt 180
 taccagcaga agcaggatc ctccccaa ccttggatt atgccccat caactggctt 240
 tctggagtc ctgctgcctt cagtggcagt gggcttgga ccttctact tctacaatc 300
 agcagatgg aggtcgaaga tgctgccact tattactgcc agcagtgag ttttaacca 360
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtgtg 420
 ggatctggag gaggctggag ctctcaggt tatctacagc agtctggggc tgacgttggt 480
 aggcctgggg cctcagtgaa gatgtcctgc aaggctcttg gctacacatt tccagttac 540
 aatattgcact gggtaaagca gacacctaga cagggtcctg aatggattgg agctatttat 600
 ccaggaatgt gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactctga 660
 gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgag 720
 gttctatttt gtgcaagagt ggtgtactat agtaactctt actgttactt cgatgtctgg 780
 gacacatttc ccaggttcac cgtctcttct gatcaggagc cccagcagcc ccaaatcttc tgacaaaact 840
 cccacattcc caccgtcccc agcacttgaa ctctcggggc gaccgtcagt ctctctcttc 900
 cccacattcc caccgttcac cctcatgac cctcagacc ctgaggtcac atgcgttggt 960
 gtggagctga ccagacaaga ccttgaggtc aagtccaact ggtacgtgga cggcgtggag 1020
 gtgcataatt ccagacaaga gccgcgggag gatcaggagc ccaaatcttc cggcgtggag 1080
 agcgtctcta ccgtcttga ccaggactgg ctgaaatgga aggaatcaca gtgcaaggtc 1140
 tccaacaaga ccttcccagc ccccatcgag aaaaactct ccaagccaa agggcagccc 1200
 ccagacacac aggtgtacac cctgccccca cctcgggagg agatgaccaa gaaccaggtc 1260
 agcctgacct gccttggtcaa aggtctctat cccagcgaca tcgctgggga gtgggagagc 1320
 aatgggcagc cggagaacaa ctacaagacc acgctctccc tgctggagtc ttttaacctc 1380
 ttctaccttc atagcaagct caccgtggag aagagcaggt ggcagcaggg gaacgtcttc 1440
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 tccccgggta aatgatcatg a
 1521

<210> 382
 <211> 1515
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

<400> 382
 aagcttgccg ccattggatt tcaagtgcag attttcagct tcctgctaag cagtgtctta 60
 gtcataattg aggtcacaat gacttcgagg gccagctcaa gtgtaagta gctgtcatct 120
 ccaggggaga aggtcacaat ctccccaa ccttggatt atgccccat caactggctt 180
 taccagcaga agcaggatc ctccccaa ccttggatt atgccccat caactggctt 240
 tctggagtc ctgctgcctt cagtggcagt gggcttgga ccttctact tctacaatc 300
 agcagatgg aggtcgaaga tgctgccact tattactgcc agcagtgag ttttaacca 360
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtgtg 420
 ggatctggag gaggctggag gatctcagc tatctacagc agtctggggc tgacgttggt 480
 aggcctgggg cctcagtgaa gatgtcctgc aaggctcttg gctacacatt taccagttac 540
 aatattgcact gggtaaagca gacacctaga cagggtcctg aatggattgg agctatttat 600
 ccaggaatgt gtgatacttc ctacaatcag ctacagcagc tgacatctga agactctgag 660
 gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgag 720

WO 2005/037989

PCT/US2003/024918

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gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgaagtctgg 780
ggcacaggga ccacggtcac gtctcttctt gatcaggagc ccaaatcttc tgacaaaact 840
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cccccaaac ccaaggacac cctcatgac tcccgagacc ctgaggtcac atgctgtgtg 960
gtggacgtga gccacgaaga ccttgaggtc aagttcaatt ggtacgtgga cggctgggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta cctgtgtgtc 1080
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cgagaaacac aggtgtacac ctgccccca ctgcagcaga tcgcccgtga gtgggaagag 1260
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ttcttctctg ccagcaagct caccgtggag aagagcaggt ggacgaggg gaactctctc 1440
tcattgctcg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tcccgggta aatga

<210> 383
<211> 1515
<212> DNA
<213> Artificial Sequence
<220>
<223> fusion polynucleotide

<400> 383
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gtcataattg ccagaggaca aattgttctc tccagctctc cagcaatctc gttctcatct 120
ccaggggaga aggttcaaat gacttgcagg gccagctcaa gttaagtta cagtgcactg 180
taccacgaga agccaggatc ctcccccaaa ccttgattt atgcccac tcactcactg 240
tctggagtcc ctgctgctt cagtggcagt gggctgtgga cctctactc tctcacaact 300
acagagatgg aggtcgaaga tgtgtccact tattaactgc agcagtgagg ttttaacca 360
cccacgttgc gtgctgggac caagctggag ctgaaagat gcggtgtgct ggcggtgtgt 420
ggatctggag gaggctggag ctctcaggct tatctacagc agtctggggc tgagctgtgt 480
agggctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact ggttaaaaga gacacctaga caggggctcg aatggaattg agctatttat 600
ccaggaaatg gtgtatactc ctacaatcag aagttaagg gcaaggccac actgactgta 660
gacaaatctt ccagcacagc ctacatgcag ctccagcagc tgacattcga agactctcgc 720
gtcataattc gtgcaagagt ggtgtactat agtaactctt actgttactt cgaatgtctg 780
ggcacaggga ccacggcac cgtcttctt gatcaggagc ccaaatcttc tgacaaaact 840
cacacatccc caccgtcccc agcactgaa ctctctgggg gaccgtcagt ctctctcttc 900
cccccaaac ccaaggacac cctcatgac tcccgagcc ctgaggtcac atgctgtgtg 960
gtggacgtga gccacgaaga ccttgaggtc aagttcaatt ggtacgtgga cggctgggag 1020
gtgcataatg ccaagacaaa gccgcgggag gacagtcaca acagcacgta cctgtgtgtc 1080
agcgtctcta ccgtcttcca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag cctctccagc cccatctcag aaaaacata ccaagccaa agggcagccc 1200
cgagaaacac aggtgtacac ctgccccca tcccgggagg agatgaccaa gaacagagct 1260
agcctgacct gcttgggtcaa aggtctctat cccagcgaca tcgctgtgga gtgggaagag 1320
aatggggcag cggagaacaa ctacaagacc acgctctccg tctgtgactc cgacggtctc 1380
ttctactctg ccagcaagct caccgtggac aagagcaggt ggacgaggg gaactcttc 1440
tcattgctcg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tcccgggta aatga

<210> 384
<211> 1515
<212> DNA
<213> Artificial Sequence
<220>
<223> fusion polynucleotide

<400> 384
aagcttgccg ccatggattt tcaagtgcag attttcagct tctgtcta cagtgttca 60
gtcataattg ccagaggaca aattgttctc tccagctctc cagcaatctc gttctcatct 120
ccaggggaga aggttcaaat gacttgcagg gccagctcaa gttaagtta cagtgcactg 180
taccacgaga agccaggatc ctcccccaaa ccttgattt atgcccac tcactcactg 240
tctggagtcc ctgctgctt cagtggcagt gggctgtgga cctctactc tctcacaact 300

WO 2005/037989

PCT/US2003/024918

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 agcagatgg aggctgaaga tgctgcacac tattactgcc agcagtggag ttttaaccaca 360
 cccacgtttc gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtgg 420
 ggaatctggag gaagtggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
 aggcctgggg cctcagtgaa gatgtctctg aaggcttctg gctacacatt taccagttac 540
 aatatgcact ggttaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaatctct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctcgc 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
 ggacacagga cctgcgtcac cgtctcttct gatcaggagc ccaaatcttc cgaacaaact 840
 cacacatccc caccgtcccc agcacctgaa ctctgggggg gaccgtcagt ctctctcttc 900
 ccccaaaac ccaaggacac cctcatgatc tcccgagacc ctgaggtcac atgcgtgggtg 960
 gtggacgtga gccacgaaga cctcagagtc aagttaacat ggtacgtgga cggcggtggag 1020
 gtgcataatg ccaagacaaa gcgcggggag gagcagtaca acagcacgta ccggtgggtc 1080
 agcgtctctc ccgtctctga ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
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 cgagaaccac aggtgtacac cctgcctcca tccggggagg agatgacca gaacacagtc 1260
 agcctgacct gcctggtcaa aggcctctat cccagcgaca tcgctggga gtggagagac 1320
 aatgggcagc cggagaaaca ctacaagacc acgcctccg tgctggactc gcagcgtctc 1380
 ttccctctcg ccagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
 tcatgctcgc tgaatgcata ggctctgcac aaccactaca cgcagaagag cctctcctcg 1500
 tccccgggta aatga 1515

<210> 385
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 385
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 80 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140 145
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270 275
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 280 285

WO 2005/037989

PCT/US2003/024918

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 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys 300 Pro Lys Asp Thr Leu
 290 295
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 320 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys 500

<210> 386
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

<400> 386
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220

WO 2005/037989

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 Met Gln Leu Ser Ser Leu Thr Ser Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn Thr Tyr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 387
 <211> 500
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> fusion polypeptide

<400> 387
 Met Asp Phe Ser Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

WO 2005/037989

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 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270 275
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 280 285 290 295
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 300 305 310 315
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 320 325 330 335
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 340 345 350 355
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 360 365 370 375
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 380 385 390 395
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 400 405 410 415
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 420 425 430 435
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Met Thr Lys Asn Gln Val
 440 445 450 455
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 460 465 470 475
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 480 485 490 495
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Ala Ser Lys Leu Thr
 500 505 510 515
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 520 525 530 535
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 540 545 550 555
 Ser Pro Gly Lys
 560 565 570 575 580 585 590 595 600

<210> 388
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

<400> 388
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 389
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

<400> 389
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 390
 <211> 44
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> 5' oligo to mutat IgG1

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<400> 390
gttggtgatac aggagcccaa atcttctgac aaaactcaca catg 44

<210> 391
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to mutate IgG1

<400> 391
gttggtgatac aggagcccaa atcttctgac aaaactcaca catctccacc gtgc 54

<210> 392
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to mutate IgG1

<400> 392
gttggtgatac aggagcccaa atcttctgac aaaactcaca catgtccacc gtccccagca 60
cct 63

<210> 393
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 393
aagcttgccg ccatggattt tcaagtgcag attttcagct tcttgctaata cagtgtctca 60
gtcataattg ccagaggaca aattgtttct tccagctctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcatctg 180
tctggagctc cgtctcgctt ctccccaaa ccttggattt atgccccatc caacctggct 240
agcagagtgg aggttgaaga tgctgccact tattactgcc agcagtgagg agtctggggc tgagctgggtg 300
ccacaggttc ggtctgggac caagctggag ctctcaggct tatctacagc gcggtggctc gggcgtgggtg 360
ggatctggag aggttgggag gatctcctgc aagggtctctg gctacacatt taccagttac 420
agccctgggg cctcagtgaa gacacctaga caaggctcagg aagttcaagg agtctgattg agctatttat 480
aatatgacct gggtaaagaa ctacaatcag ctacatgcag ctacagcagg agtcaactctt ccaaatcttc tgacaaaact 540
ccaggaatag gtgatacttc ctacatgcag ctacagcagg agtcaactctt ccaaatcttc tgacaaaact 600
gacaaatcct ccagcacagc ctacatgcag ctacagcagg agtcaactctt ccaaatcttc tgacaaaact 660
gtctatttct gtgcaagagt ggtgtactat agtaactctt ctacagcagg agtcaactctt ccaaatcttc tgacaaaact 720
ggcacaggga ccacggtcac cgtctcttct gatcaggagg cctctggggg gaccgtcagt ctctctcttc 780
cacacatgac caccgtgccc cctcatgata tcccggagccc ctgaggtcac atgcgtgggtg 840
cccccaaaac ccaaggacac cctgagggtc aagttcaact ggtacgtgga cggcgtggag 900
gtggacgtga ccacgaaga gccgcgggag gagcagtaca acagcagcta cgtgtgggtc 960
gtgcataatg ccaagacaaa ccaggactgg ctgaatggga agagagtaca gtgcaaggctc 1020
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cgagaaccac aggtgtacac cgtgtcttat ccagcgaca tgcgctgga gtggagagctc 1200
agcgtgacct cgaggaacaa ctacagagac caccgtggag aagagcaggt ggcagcaggg 1260
aattgggacct cgtctctctc acagcaagct caccgtggag aagagcaggt ggcagcaggg 1320
ctatgctctc tgatgatga ggtctctgac aaccactata cgcagaagag cctctctctg 1380
ctatgctctc tgatgatga ggtctctgac aaccactata cgcagaagag cctctctctg 1440
ctatgctctc tgatgatga ggtctctgac aaccactata cgcagaagag cctctctctg 1500

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WO 2005/037989

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
tctccgggta aatgatctag a 1521

<210> 394
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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gtcataattg ccagaggaca aattgtttct tccagctctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgctctgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcaaatc 300
agcagagtgg aggtctgaaga tgctgccact tattactgcc agcagtgagg ttttaacca 360
cccacgtlct ggtctgggac caagctggag ctctcaggct tatctacagc agtctgggct gggcggtgg 420
ggatctggag gaggtgggag gatgtctctg aagggctctg gctacacatt taccagttac 480
agggctgggg cctcagtgaa gacacttaga aggttcaagg ctacacatt taccagttac 540
aatgtccact gggtaaagca ctacaatcag atgtctcagg gctacacatt taccagttac 600
ccaggaaagt gtgatacttc ctacacttaga aggttcaagg ctacacatt taccagttac 660
gacaaatcct ccagcacagc ctacacttaga aggttcaagg ctacacatt taccagttac 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt tgacaaact 780
ggcacaggga gccaggtcac cgtctcttct gatcaggagc ccaaatcttg tgaacaaact 840
cacacatctc caccgtgcc agcacctgaa ctctctgggg gaccgtcagt ctctctcttc 900
cccccaaac ccaaggacac cctcatgact tcccggaccc ctgaggtcac atgcgtgtg 960
gtggactgga gccacgaaga cctgaggtc aagtccaact ggtactgtga cggcggtgag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtggtc 1080
agcgtctctca ccgtctctga ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tcccaaaaag cctctccagc cccatcgag aaaaacaatc ccaaggccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgcgcaa gaacacagct 1260
agctgtacct gctcgttcaa aggtcttctat cccagcgaca tcgctgtgga gtggagagtc 1320
aatgggcagc cgggaagcaa ctacaagacc acgcctcccg tgcgtgactc cgacagcttc 1380
ttcttctctc acagcaagc caccgtggag aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgtcccg tgatgcata ggtcttcgac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatgatctag a 1521

<210> 395
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 395
aagcttgccg ccatggattt tcaagtgcag attttcagct tctctgtaat cagtgtctta 60
gtcataattg ccagaggaca aattgtttct tccagctctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgctctgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt ggggtctggga cctcttactc tctcaaatc 300
agcagagtgg aggtctgaaga tgctgccact tattactgcc agcagtgagg ttttaacca 360
cccacgtlct ggtctgggac caagctggag ctctcaggct tatctacagc agtctgggct gggcggtgg 420
ggatctggag gaggtgggag gatgtctctg aagggctctg gctacacatt taccagttac 480
agggctgggg cctcagtgaa gatgtctctg aagggctctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga aagttcaagg gcaaggccac actgacttga 600
ccaggaaagt gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgacttga 660
gacaaatcct ccagcacagc ctacacttaga aggttcaagg ctacacatt taccagttac 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacgttcc agcacctgaa ctcttcttct gatcaggagc gaccgtcagt ctctctcttc 900
cacacatgct caccgtcccc agcacctgaa ctcttgggct tcccggagcc ctgaggtcac atgcgtgtgg 960
cccccaaac ccaaggacac cctcatgact ctcttgggct ctgaggtcac atgcgtgtgg 1020
gtggcagtgga gccacgaaga cctgaggtc gagcagtaca acagcacgta ccgtgtgggtc 1080
gtgcataatg ccaagacaaa gccgcgggag

WO 2005/037989

PCT/US2003/024918

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 cgagaaccac aggtgtacac cctgcgccca tcccgggatg agctgaccac gaaccaggtcc 1260
 accctgacct gcctgtgtcaa aggtctctat cccagcgaca tcgctgtgga gtgggagagc 1320
 aatgggcagc cggagaacaa ctacaagacc acgctcccg tgctggactc cgacggctcc 1380
 ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
 tcatgctcgg tgatgcatga ggtctctgac aaccactaca gcgagaagag cctctccctg 1500
 tctccgggta aatgatctag a

<210> 396
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

<400> 396
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Val Ser Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

WO 2005/037989

PCT/US2003/024918

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 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 397
 <211> 500
 <212> PRT
 <213> Artificial sequence
 <220>
 <223> fusion polypeptide

<400> 397
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Cys Asp Lys Thr His Thr Ser Pro Pro Cys Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

WO 2005/037989

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 Ser Pro Gly Lys
 325 330 335
 340 345 350
 355 360 365
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 415 420
 425 430
 435 440
 445 450
 455 460
 465 470
 475 480
 485 490
 495 500

<210> 398
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

<400> 398
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 Asp Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 1 5 10 15
 20 25 30
 35 40 45
 50 55 60
 65 70 75
 80 85 90
 95 100
 105 110
 115 120
 125 130
 135 140
 145 150
 155 160
 165 170
 175 180
 185 190
 195 200
 205 210
 215 220
 225 230
 235 240
 245 250
 255

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260 265 270
 Cys Asp Lys Thr His Thr Cys Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Ser
 320 325 330
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 335 340 345
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 350 355 360
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 365 370 375
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 380 385 390
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 395 400
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 405 410 415
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 420 425 430
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 435 440 445
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 450 455 460
 Met His Glu Ala Leu His Asn His Thr Gln Lys Ser Leu Ser Leu
 465 470 475
 Ser Pro Gly Lys
 480 485 490 495 500

<210> 399
 <211> 793
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 399
 atgttgatata catctcagct ccttgggctt ttactcttct ggatttcagc ctccagaagt 60
 gacatagtgc tgactcagac tccagccact ctgtctctaa ttcctggaga aagagtccaca 120
 atgacctgtga agaccagtcga gaattattggc acaatcttac actggtatca ccaaaaacca 180
 aaggaggctc caagggtctt catcaagtat gcttcgcagt ccattctcgg gatccccttc 240
 agattcagtg gcagtggttc gaaacacagat ttactctcta gcatcaataa cctggagcct 300
 gatgatatcg gaattatata ctgtcaacaa agtagaagct ggcctgtcac gttcggctct 360
 ggacacaaag tggagataaa acgggggtggc ggtggctcgg gcggaggtag gtcgggtggc 420
 ggcgagatctc aggtcaagct ttacagctac taggggaacc tggggcctca 480
 ctgaaactgt cctgcaagac cctgcagtag agtaggaag atcactatat ttcttgggtg 540
 aaacagaagc ctggagaag ctaggcaagc ggttctgaac ttatgggtgg aaatgggtgg 600
 acaagctaca atcaaaaatt ccagggcaag gcttagataa aatctctagc 660
 acagcctaca tggaaactcag cagcctgaca tctgaggatt ctgccatcta ttactgtgca 720
 agaagggcgg tagcgacggg ccattgctatg gactactggg gtcaggggat ccaagtacc 780
 gtctctcctg atc 793

<210> 400
 <211> 264
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

WO 2005/037989

PCT/US2003/024918

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<400> 400
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe Trp Ile Ser
1 5 10 15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
20 25 30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
35 40 45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
50 55 60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
85 90 95
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
100 105 110
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
130 135 140
Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser
145 150 155 160
Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr
165 170 175
Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly
180 185 190
Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln
195 200 205
Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met
210 215 220
Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
225 230 235 240
Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255
Ile Gln Val Thr Val Ser Ser Asp
260

<210> 401
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 401
gttgttgatc agccagttcc ctcaactcca cctacc

36

<210> 402
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 402
gttgtttttcg aagatccgc gtccacctcc gccatgacaa caga

44

<210> 403
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<223> oligonucleotide primer

<400> 403
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<210> 404
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 404
gtgttagat ctggagccca aatcttgta caaaactcac acatg 45

<210> 405
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 405
gtgtggatc cttcgaacc gttcctggg ctgctgcact cgggtgctg 48

<210> 406
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 406
gtgttatcg atctcgagtt atcaggacgc ttcggaggta gatgcgtc 48

<210> 407
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 407
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cgctgacaga ggcgcctaga cctcttctcc atgctgctgg agcagaacga cctggagccc 180
gggcacacgc agctcctcgc cgagctgctc gcctccctgc ggcgccacga cctgtctcgg 240
cgctcgacgc acttcgaggc gggggcgcg cgccctggga agaagacctg 300
tgtgcagcat ttaacgtcat atgtgataat gtggggaag attggagaag gctggtcgt 360
cagctcaag tctcagacac caagatcgac agcatcgagg acagataccc ccgcaacctg 420
acagagctg tgcgggagtc actgagaatc tgggaagaaca cagagaagga gaacgcaaca 480
gtggccaccc tgggggggct tctcaggtcc tgcagatga acctggtggc tgacctgtgta 540
caagaggttc agcagggcgc tgacctccag aacaggagtg gggccatgtc cccgatgtca 600
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<210> 408

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 408

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Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly
 20          25          30
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
 35          40          45
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
 50          55          60
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
 65          70          75
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly
 80          85          90
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
100          105          110
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
115          120          125
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
130          135          140
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
145          150          155
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
160          165          170
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
175          180          185
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser
190          195          200
Glu Ala Ser
210

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<210> 409

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 409

gttgaggatc ctcccttttg ggtgctgggt gtgggtgggt tcctggcttg ctatagcttg 60

<210> 410

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 410

gtgtttcga acccagaaaa taataaaggc cactgttact agcaagctat agcaagccag 60

<210> 411

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

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WO 2005/037989

PCT/US2003/024918

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<400> 411
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<210> 412
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 412
gttgtttcga acccgaaaa taataaaggc cac                                     33
<210> 413
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 413
gttgaggatc ctctgctcc catcctgg                                         28
<210> 414
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 414
gttgtttcga acggcaaaag agtaggtcag gc                                     32
<210> 415
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 415
gttgaggatc cttcgaacc attcctggtg ctgctgcact cgctg                     45
<210> 416
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 416
gttgttatcg atctcgagtc aggggtgttc tgaggaagac ac                       42
<210> 417
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 417

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WO 2005/037989

PCT/US2003/024918

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gtggatcctt cgaacatgga cccattcctg gtgctgctgc actcgctgctc cggcagcctg 60
tcgggcaacg atctgatgga gctcaagttc ttgtgcccgc agcgcgtgag caaacgaaag 120
ctggagcgcg tgcagagtgg cctggacctg ttacgggtgc tgcctggaagca gaacgacctg 180
gagcgcgggc acaccgggctt gctgcccagc ttgtctgctc cgtgcccgcg acacgatcta 240
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gattctcagg tggcatttga catttgttgt gacaaatggtg ggagagactg gaaaagactg 360
gcccgcgagc tgaaggtgtc tgaggccaag atggatggga ttgaggagaa gtacccccga 420
agtctgagtg agcgggttaag ggagagctctg aaagtctgga agaattgctga gaagaagaac 480
gcctcggttg cggacttggt caagcgctg cggacctgca ggctgaattc ggtggctcag 540
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gattcaactg tgtcttcttc agaaaacccc tgactcgaga tcgat 645

<210> 418
<211> 210
<212> PRT
<213> Artificial sequence

<220>
<223> fusion polypeptide

<400> 418
Val Asp Pro Ser Asn Met Asp Pro Phe Leu Val Leu Leu His Ser Leu
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Ser Gly Ser Leu Ser Gly Asn Asp Leu Met Glu Leu Lys Phe Leu Cys
20 25 30
Arg Glu Arg Val Ser Lys Arg Lys Leu Glu Arg Val Glu Ser Gly Leu
35 40 45
Asp Leu Phe Thr Val Leu Leu Glu Glu Asn Asp Leu Glu Arg Gly His
50 55 60
Thr Gly Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu
65 70 75 80
Leu Glu Arg Leu Asp Asp Phe Glu Ala Gly Thr Ala Thr Ala Ala Pro
85 90 95
Pro Gly Glu Ala Asp Leu Glu Val Ala Phe Asp Ile Val Cys Asp Asn
100 105 110
Val Gly Arg Asp Trp Lys Arg Leu Ala Arg Glu Leu Lys Val Ser Glu
115 120 125
Ala Lys Met Asp Gly Ile Glu Glu Lys Tyr Pro Arg Ser Leu Ser Glu
130 135 140
Arg Val Arg Glu Ser Leu Lys Val Trp Lys Asn Ala Glu Lys Lys Asn
145 150 155 160
Ala Ser Val Ala Gly Leu Val Lys Ala Leu Arg Thr Cys Arg Leu Asn
165 170 175
Leu Val Ala Asp Leu Val Glu Glu Ala Glu Glu Ser Val Ser Lys Ser
180 185 190
Glu Asn Met Ser Pro Val Leu Arg Asp Ser Thr Val Ser Ser Ser Glu
195 200 205
Thr Pro
210

<210> 419
<211> 48
<212> DNA
<213> Artificial sequence

<220>
<223> oligonucleotide

<400> 419
gtttggatc cttcgaacat ggagaacaac aaaacctcag tggattca

48

<210> 420
<211> 44
<212> DNA
<213> Artificial Sequence

WO 2005/037989

PCT/US2003/024918

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
<220>
<223> oligonucleotide

<400> 420
gttggtatcg atctcgagct agtgataaaa gtacagttct ttgcg          44
<210> 421
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 421
gttggttcga acatggattt ccagagttgt cttatgcta ttgctg          46
<210> 422
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 422
gttggtatcg atctcgagtc attagggagg gaagaagagc ttcttcgc          48
<210> 423
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 423
gttggtggtc cttcgaacat ggagaacact gaaaactcag tggat          45
<210> 424
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 424
gttggtatcg atctcgagtt agtgataaaa atagagttct tttgtgag          48
<210> 425
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 425
gttggtggtc cttcgaacat ggacttcagc agaaatcttt atgat          45
<210> 426
<211> 48

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WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 426

gttggtatcg atgcatgctc aatcagaagg gaagacaagt ttttttct

48

18

EXPRESS MAIL NO:

1